Breast cancer is the most common neoplasia in women. Despite important advances in treatment, metastatic breast cancer is incurable and new treatments to improve patient outcome are needed. Therefore, identification of the key molecular alterations that induce proliferation or drug resistance in breast cancer cells will be helpful in defining potential therapeutic targets.

Tyrosine kinases, either cytosolic (soluble) or transmembrane (membrane-bound), play important roles in animal physiology, and their deregulation has been linked to the development and progression of different types of cancer (1,2). In breast cancer, overexpression of the HER2 (also known as v-erb-b2 erythroblastic leukemia viral oncogene homolog 2), a receptor tyrosine kinase (RTK) (2), occurs in approximately 25% of patients and is associated with shorter survival (3). These findings led to several preclinical studies that confirmed the oncogenic potential of HER2 (4–7) and also led to the development of therapeutic agents targeting HER2 (2). One of these compounds is trastuzumab—a humanized monoclonal antibody that binds to the extracellular domain of HER2 (8,9). In HER2-overexpressing breast tumors, treatment with trastuzumab in combination with other antineoplastic drugs increases patient survival in metastatic and early-stage breast cancer (10,11). Despite the effectiveness of such treatments, a substantial number of HER2-positive patients do not respond to trastuzumab or relapse in a short period of time (12). Therefore, the development of novel therapeutic strategies that are aimed at increasing the efficacy of trastuzumab may help in preventing or delaying relapse in patients with HER2-positive tumors (12). In this context, the combined targeting of HER2 and other tyrosine kinases provides new avenues for the treatment of HER2-positive breast cancer patients.

**Effect of Multikinase Inhibitors on Caspase-Independent Cell Death and DNA Damage in HER2-Overexpressing Breast Cancer Cells**

Samuel Seoane, Juan Carlos Montero, Alberto Ocaña, Atanasio Pandiella

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Correspondence to: Atanasio Pandiella, MD, PhD, Instituto de Biología Molecular y Celular del Cáncer-CSIC, Campus Miguel de Unamuno, 37007-Salamanca, Spain (e-mail: atanasio@usal.es).

**Background**

The receptor tyrosine kinase, HER2, is overexpressed in approximately 25% of patients with breast cancer and is implicated in the aggressiveness of cancer. Targeting of HER2 signaling with trastuzumab, a monoclonal antibody that inhibits HER2 activity, has demonstrated clinical benefits.

**Methods**

We investigated whether the antitumor activity of trastuzumab can be potentiated by dasatinib, a small-molecule tyrosine kinase inhibitor, on breast cancer cell lines that overexpress HER2 (BT474 and SKBR3) or have normal HER2 expression (MCF7 and T47D). Functional, biochemical, and gene expression microarray studies were performed to test the effect of trastuzumab, dasatinib, or a combination of trastuzumab and dasatinib on cell proliferation; HER activation; cell cycle; DNA damage; and apoptosis. The effect of drugs on mice (n = 6 per group) bearing xenograft tumors originating from HER2-overexpressing BT474 cells was assessed, and tumors were evaluated for an effect on volume, HER signaling, and DNA damage. All statistical tests were two-sided.

**Results**

Trastuzumab and dasatinib combination showed a synergistic effect on the proliferation of HER2-overexpressing breast cancer cells (combination index = 0.44, 95% confidence interval = 0.30 to 0.58). The drug combination also induced a stronger inhibitory effect on HER2 activation than the individual drugs, decreased the level of proteins involved in DNA damage response, induced DNA double-strand breaks, cell cycle arrest, and caspase-independent apoptosis. Mice (n = 6 per group) bearing xenograft tumors originating from HER2-overexpressing BT474 cells showed statistically significantly reduced tumor volume on day 28 when treated with the drug combination (control vs trastuzumab and dasatinib combination; mean volume = 2.6 vs 0.5 cm³, difference = 2.1 cm³, 95% confidence interval = 0.76 to 3.51 cm³, P = .01) and total regression of tumors by day 36 with no later relapse.

**Conclusions**

Results showed that HER2 and dasatinib-sensitive tyrosine kinases act in a synergistic manner to safeguard the breast cancer cells from DNA damage. The therapeutic targeting of multikinase inhibition opens new avenues for the treatment of HER2-positive breast cancer patients.

kinases presents an interesting strategy because these tyrosine kinases are associated with breast cancer tumorigenesis and are of substantial interest as potential drug targets (12). The insulin-like growth factor 1 receptor (IGF-1R), an RTK, has been shown to increase the growth of breast cancer cells and is also implicated in developing resistance to trastuzumab (13). Indeed, cotargeting of IGF-1R and HER2 offers an important advantage over targeting of the individual RTKs in breast cancer cells (14). The v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (c-KIT) RTK is overexpressed in triple-negative breast cancers (those that do not express estrogen receptor, progesterone receptor, and HER2) (15). The activation of two nonreceptor cytosolic tyrosine kinases, c-abl oncogene 1 (ABL1) and c-SRC tyrosine kinase (CSK), is associated with the aggressiveness of breast cancer (16) and proliferation of triple-negative breast cancers (16,17), respectively. Moreover, c-SRC has also been associated with antiestrogen resistance in estrogen receptor–positive breast tumors (18).

Dasatinib, a small-molecule tyrosine kinase inhibitor, has been shown to target the cytosolic c-SRC and ABL1 kinases, as well as the RTKs c-KIT and platelet-derived growth factor receptors alpha and beta (17,19–21). The reported biological activity of dasatinib against triple-negative breast cancer (17,20), together with its favorable antitumoral activity in head and neck cancer when combined with gefitinib (22), led us to explore whether dasatinib could increase the antitumoral effect of trastuzumab on HER2-positive breast cancers.

In this study, we investigated the effects of trastuzumab and dasatinib combination on HER2 activation and HER2-mediated signaling using biochemical and gene expression microarray analyses and determined the effectiveness of the drug combination in preclinical mouse models.

**Materials and Methods**

**Reagents and Antibodies**

Cell culture medium (Dulbecco’s modified Eagle medium (DMEM)) and serum (fetal bovine serum [FBS]) were purchased from Invitrogen (Gaithersburg, MD). Protein A-Sepharose was from GE Healthcare Life Sciences (Piscataway, NJ). Immobilon-P membranes were from Millipore Corporation (Bedford, MA). Nitrocellulose membranes were from Bio-Rad Laboratories (Hercules, CA). Trastuzumab and dasatinib were from Roche Diagnostics (Barcelona, Spain) and Bristol-Myers Squibb (Princeton, NJ), respectively. Other generic chemicals were purchased from Sigma-Aldrich (St Louis, MO), Roche Biochemicals (Hoffmann, Germany), or Merck (Darmstadt, Germany). The caspase inhibitors (Z-IETD-FMK, Z-LEHD-FMK, and Z-VAD-FMK) were obtained from BD Biosciences (San Jose, CA).

The following antibodies were purchased from Santa Cruz Biotechnology (Santa Cruz, CA)—rabbit polyclonal anti-HER3 antibody (raised against the carboxyl [C] terminus of human HER3; 1 µg/mg of protein lysate for immunoprecipitation, 0.1 µg/dot for dot blot, and 1:5000 dilution for immunoblot studies); mouse monoclonal IgG2a anti-HER4 (raised against an epitope mapping between amino acids 1280–1308 at the C terminus of human HER4; 1 µg/mg of protein lysate for immunoprecipitation, 0.1 µg/dot for dot blot, and 1:5000 dilution for immunoblot studies); mouse monoclonal IgG2b anti-phosphotyrosine (clone PY99; 1:10000 dilution); rabbit polyclonal IgG anti–myeloid cell leukemia sequence 1 (MCL1) (raised against an epitope mapping within an internal region of human MCL1; 1:2000 dilution); rabbit polyclonal anti–baculoviral IAP repeat-containing 2 protein (BIRC2, also known as c-IAP-1 inhibitor of apoptosis protein 1) (raised against an epitope corresponding to amino acids 111–193 mapping within an internal region of human BIRC2; 1:2000 dilution); mouse monoclonal anti–glyceraldehyde-3-phosphate dehydrogenase (1:10 000 dilution); rabbit polyclonal IgG anti–myeloid cell leukemia sequence 1 (MCL1) (raised against an epitope mapping within an internal region of human MCL1; 1:2000 dilution); mouse monoclonal anti–glyceraldehyde-3-phosphate dehydrogenase (1:10 000 dilution); rabbit polyclonal anti–protein tyrosine kinase inhibitor reported to have antigrowth activity in breast cancer cells, showed greater inhibition of breast cancer cell proliferation and tumor development.

**Contribution**

Trastuzumab and dasatinib combination showed a synergistic effect on the inhibition of HER2-overexpressing breast cancer cell proliferation and a complete regression of tumor xenografts in the in vivo mouse model with no relapse after treatment discontinuation.

**Implications**

The antitumor activity of trastuzumab can be potentiated by dasatinib in HER2-positive tumors.

**Limitations**

The efficacy of the drug combination in a mouse model is not indicative of clinical success. In addition, whether an effective dose of the drug combination has an adverse effect in humans is not known.

*From the Editors*
reacts with both human ERK1 and ERK2; 1:10000 dilution); mouse monoclonal IgG2a anti–cyclin-dependent kinase-2 (CDK2) (raised against human recombinant CDK2; 1:1000 dilution); rabbit polyclonal anti–cyclin-dependent kinase inhibitor 1A (CDKN1A, also known as p21) (raised against the C terminus of human p21; 1:5000 dilution); rabbit polyclonal anti–cyclin-dependent kinase inhibitor 1B (CDKN1B, also known as p27) (raised against the C terminus of human p27; 1:5000 dilution); rabbit polyclonal anti–cyclin-dependent kinase inhibitor 2B (CDKN2B) (1:2000 dilution); rabbit polyclonal anti-HER2 antibody (clone Ab-3, raised against amino acids 1242–1255 at the C terminus of human HER2; 1 µg/mg of protein lystate for immunoprecipitation, 0.1 µg/dot for dot blot, and 1:10000 dilution for immunoblotting) was purchased from Calbiochem (La Jolla, CA); cetuximab, the anti–epidermal growth factor receptor (EGFR) (also known as HER1) antibody (1 µg/mg of protein lystate for immunoprecipitation and 0.1 µg/dot for dot blot), was purchased from Merck (Madrid, Spain). A polyclonal anti-EGFR antibody (raised against the amino acids 909–1210 of the C terminus of human EGFR, dilution 1:5000 for immunoblotting) was raised in our laboratory (23).

The following rabbit polyclonal antibodies were purchased from Cell Signalling Technology (Beverly, MA)—anti–phosphorylated (Tyr1248) HER2 (1:10000 dilution); anti–phosphorylated (Tyr416) SRC (1:10000 dilution); anti–phosphorylated (Tyr421/Ser424) ribosomal protein S6 kinase, 70 kDa, polypeptide 2 (RPS6KB2, also known as p70S6K) (1:5000 dilution); anti–phosphorylated (Ser136) BCL2-associated agonist of cell death (BAD) (1:1000 dilution); and anti–phosphorylated (Ser139) H2A histone family, member X (H2AFX, also known as H2AX, and its phosphorylated form at this site is known as γH2AX) (1:1000 dilution). The rabbit polyclonal anti-BAD antibody (clone 11E3; 1:1000 dilution) and the mouse monoclonal anti–phosphorylated (Ser1981) ataxia telangiectasia mutated (clone 10H11.E12; 1:1000 dilution) were also purchased from Cell Signalling Technology.

The following antibodies were purchased from BD Biosciences—the mouse monoclonal anti-caspase-3 (CASP3) (clone 19, raised against amino acids 1–219 of human caspase 3; 1:20000 dilution); mouse monoclonal anti-caspase-8 (CASP8) (clone 3-1-9, raised against full-length recombinant human caspase 8; 1:10000 dilution); mouse monoclonal anti-caspase-9 (CASP9) (clone 2-22, raised against amino acids 1–134 of human caspase-9; 1:10000 dilution); mouse monoclonal anti–B-cell CLL/lymphoma 2 (BCL2) (clone 6C8, raised against human recombinant BCL2; 1:20000 dilution); rabbit polyclonal anti–BCL2-like 1 (BCL2L1, also known as BCL-X) (raised against amino acids 18–233 of human BCL2L1; 1:5000 dilution); and mouse monoclonal anti–phosphorytosine-horseradish peroxidase (HRP) (clone PY20; 1:10000 dilution).

The following antibodies were purchased from Jackson ImmunoResearch Laboratories, Inc (West Grove, PA); Alexa 488-conjugated antibody was from Invitrogen; HRP conjugates of anti-rabbit and anti-mouse IgG were from Bio-Rad Laboratories; rabbit polyclonal anti-calnexin antibody was from Stressgen Biotechnologies Corporation (Victoria, Canada); and anti–phosphorylated human AKT (Serine 473) antibody was raised in our laboratory against the amino acid sequence RPHFPQFSpS473YSAS (p = phosphorylated).

Cell Culture

Four breast cancer cell lines—BT474, SKBR3, MCF7, and T47D—were grown in DMEM supplemented with 10% FBS, 100 mU/mL penicillin (Invitrogen), 100 µg/mL streptomycin (Invitrogen), and 2 mM l-glutamine (Invitrogen) in a 5% CO₂ atmosphere at 37°C. The cell lines were obtained from the American Type Culture Collection Cell Biology Collection (Manassas, VA). The BT474 and SKBR3 cell lines overexpress HER2 receptor, whereas MCF7 and T47D cell lines have normal HER2 expression (24). The level of HER2 proteins in these cell lines was verified by immunoblotting (Supplementary Figure 1, available online).

For three-dimensional cell culture, 12-mm coverslips were coated with 60 µL of ice-cold Matrigel (BD Biosciences) and incubated at 37°C for 20 minutes to allow the Matrigel to solidify. Cells were treated for 5 minutes with 0.25% trypsin–EDTA solution (2.5 g/L of trypsin, 0.38 g/L of EDTA) (Invitrogen). A single-cell suspension containing 5 × 10³ cells per 100 µL volume of medium, supplemented with 2% (vol/vol) of Matrigel, was carefully placed on top of the solidified Matrigel. Incubation was carried out at 37°C for 30 minutes to allow the cells to attach to the Matrigel. The coverslips were then placed in six-well plates, 500 µL of medium was added per well, and the cells were cultured for 10 days. Cells were then treated with different drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination of 10 nM trastuzumab and 1 µM dasatinib) for 1 week. Selection of the combination dose of trastuzumab was based on previously reported data (14). Phase contrast photographs of cells as monolayers, or in three-dimensional cultures, were taken with a Nikon Eclipse Ti-S inverted microscope (Izasa, Barcelona, Spain). The microscope was equipped with a ProgRes C3 camera and the ProgRes CapturePro 2.7 software, purchased from Jenoptik (Jena, Germany). Quantitation of the sphere diameters was performed manually by tracing a straight line across the diameter of the sphere and scoring its value as arbitrary length units. Two hundred spheres were scored for each condition, and the mean and 95% confidence interval (CI) values were calculated.

Immunoprecipitation and Immunoblotting

BT474, SKBR3, MCF7, and T47D cells were grown in DMEM with 10% of FBS and at 80% confluence (2 days later) were treated with drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination...
of 10 nM trastuzumab and 1 µM dasatinib) for 48 hours. Cells were washed with phosphate-buffered saline (PBS) (137 mM NaCl, 2.7 mM KCl, 8 mM NaHPO₄, 1.5 mM KH₂PO₄) and lysed in ice-cold lysis buffer (20 mM Tris–HCl [pH 7.0], 140 mM NaCl, 50 mM EDTA, 10% glycerol, 1% Nonidet P-40, 1 µM pepstatin, 1 µg/mL aprotinin, 1 µg/mL Leupeptin, 1 mM phenylmethyl sulfonyl fluoride, 1 mM sodium orthovanadate). Lysates were centrifuged at 10 000g at 4°C for 10 minutes, and supernatants were treated with the corresponding antibody and protein A-Sepharose. Immunoprecipitations were performed at 4°C for at least 2 hours; immune complexes were recovered by a short centrifugation at 10 000g for 15 seconds, followed by three washes with 1 mL cold lysis buffer. Samples were then boiled in electrophoresis sample buffer and placed on 6%–15% sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) gels, depending on the molecular weight of the proteins to be analyzed. Immunoblotting was performed as previously described (25). Briefly, after electrophoresis, proteins in gels were transferred to polyvinylidene difluoride membranes (Millipore Corporation). Membranes were blocked in Tris-buffered saline with Tween (TBST) (100 mM Tris [pH 7.5], 150 mM NaCl, 0.05% Tween 20) containing 1% bovine serum albumin for 1 hour and then incubated with the corresponding antibody for 2–16 hours. After washing with TBST, membranes were incubated with HRP-conjugated anti-mouse or anti-rabbit secondary antibodies (1:10 000 dilution) for 30 minutes and bands were visualized by using ECL Plus Western Blotting Detection System (GE Healthcare, Buckinghamshire, United Kingdom).

**Dot Blots and Antibody Arrays**

For dot blots, each antibody (0.1 µg) was adsorbed onto a nitrocellulose membrane. The membrane was dried at room temperature for 30 minutes and then blocked for 2 hours in TBST containing 5% bovine serum albumin. The membranes were then incubated with 1 µg of protein lysates overnight at 4°C. The membranes were washed in TBST three times and incubated for 2 hours with the anti-phosphotyrosine-HRP antibody (1:5000 dilution). After three washes of 10 minutes each in TBST, membranes were incubated with the ECL Plus Western Blotting Detection System. The BT474 cell lysates were used as the positive control, as they contain high levels of resting tyrosine phosphorylation of several cellular proteins (26).

To perform the dot blot analyses with commercial arrays, we used the human phospho-RTK array kit (R&D Systems, Abingdon, United Kingdom) and followed the manufacturer’s instructions.

**Cell Surface Biotinylation and Cell Fractionation**

For cell surface biotinylation, BT474 cells (2 × 10⁶ cells per 100-mm dishes) were cultured in DMEM supplemented with 10% FBS, until the cells reached 80% confluence. Cells were then treated with different drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination of 10 nM trastuzumab and 1 µM dasatinib) for 48 hours. Cell monolayers were washed twice with ice-cold Krebs–Ringer–HEPES (KRH) (129 mM NaCl, 5 mM NaHCO₃, 4.8 mM KCl, 1.2 mM KH₂PO₄, 1 mM CaCl₂, 1.2 mM MgCl₂, 2.8 mM glucose, 10 mM HEPES free acid [pH 7.4]) and then incubated with N-hydroxysulfosuccinimide-LC-biotin (Thermo Scientific Pierce Protein Research Products, Rockford, IL) (100 µg/mL) for 2 hours at 4°C. Cells were washed again with KRH and then incubated with KRH containing 10 mM glycine for 15 minutes at 4°C. Cell monolayers were washed and lysed, and the lysates were precipitated with anti-HER2 antibodies. Samples were subjected to 8% SDS-PAGE gels and analyzed by immunoblotting using streptavidin–HRP secondary antibody (Sigma-Aldrich).

For cell fractionation experiments, BT474 cells were cultured as above in 100-mm dishes, washed with PBS, incubated in cell dissociation buffer (0.25 M sucrose, 1 mM EDTA, 1 mM phenylmethyl sulfonyl fluoride, and 10 mM Tris–HCl [pH 7.0]) for 10 minutes at 37°C. The cell suspension was homogenized on ice with a tight-fitting Dounce homogenizer (50 strokes) (Kontes Glass Company, Vineland, NJ). This homogenate was centrifuged at 4000g for 10 minutes. The resulting pellet was resuspended (50 strokes) and centrifuged at the same speed. The supernatants from these two centrifugation steps were pooled and centrifuged at 30 000g for 30 minutes. The supernatant was taken as the cytosolic fraction and the pellet as the microsomal fraction.

**MTT metabolization, Cell Cycle, and Apoptosis Assays**

Cell proliferation experiments were carried out using 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assays, where MTT is reduced to purple formazan by the mitochondria of living cells. Increase in cell number is detected by augmented MTT metabolization, and decrease in cell number is reflected by decrease in MTT metabolization. BT474, SKBR3, MCF7, and T47D cells were plated at a density of 1 × 10⁵ cells per well in 24-well plates and cultured overnight in DMEM supplemented with 10% FBS. Each well was replaced with 250 µL of fresh medium containing MTT (0.5 µg/µL) and incubated for 1 hour. The medium was then removed and 500 µL of dimethyl sulfoxide was added to each well. The plate was agitated in the dark for 5 minutes to dissolve the MTT-formazan crystals. The absorbance of the samples was recorded at 570 nm in a multwell plate reader (Tecan ULTRA Evolution, Männedorf, Switzerland). The first measurement was performed 24 hours after the cells were plated and before the addition of the drugs. This value was considered to be the baseline value. Then, drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination of 10 nM trastuzumab and 1 µM dasatinib) were added to the respective wells, and MTT measurements were performed at 2, 3, and 5 days after treatment. In case of dasatinib, we used three doses (0.1, 1, and 10 µM) to plot the dose–response curves in all four breast cancer cell lines. The selected doses were one order of magnitude above (10 µM) and below (0.1 µM) the dose of dasatinib (1 µM) previously found to be effective in triple-negative breast cancer cell lines (17) and also spanned the dose range that previously showed inhibition of proliferation in a large panel of cancer cell lines (20). Results were plotted as the mean (95% CI) values of quadruplicates from a representative experiment that was repeated at least two independent times.

For cell cycle analyses, BT474 cells were cultured in 100-mm culture dishes, grown to 50%–70% confluence, and treated with drugs (10 nM trastuzumab in PBS, 1 µM dasatinib in dimethyl sulfoxide [final dimethyl sulfoxide concentration 1:1000], or a combination of 10 nM trastuzumab and 1 µM dasatinib) for 2 hours at 4°C. Cells were washed again with KRH and then incubated with KRH containing 10 mM glycine for 15 minutes at 4°C. Cell monolayers were washed and lysed, and the lysates were precipitated with anti-HER2 antibodies. Samples were subjected to 8% SDS-PAGE gels and analyzed by immunoblotting using streptavidin–HRP secondary antibody (Sigma-Aldrich).
84 hours. Cell monolayers were then incubated in trypsin–EDTA and resuspended in 1 mL of PBS. After three washes with PBS, the cell pellets were resuspended in 70% ethanol and incubated for 30 minutes at 4°C. Cells were centrifuged at 153g, and cell pellets were treated with 1 mL of propidium iodide (PI) staining solution (PBS containing 50 µg/mL of PI, 0.5% Tween 20, 0.1 µg/mL RNase A) (Sigma-Aldrich). DNA content and cell cycle analyses were performed by using a FACScalibur flow cytometer and the CellQuest software (BD Biosciences).

For apoptosis analyses, BT474 cell monolayers were incubated in trypsin–EDTA, washed twice with cold PBS, and then resuspended in binding buffer (10 mM HEPES free acid [pH 7.4], 140 mM NaCl, 2.5 mM CaCl\(_2\)) at a concentration of 1 × 10\(^6\) cells per mL. A total of 1 × 10\(^6\) cells were incubated for 15 minutes in the dark with Annexin V-fluorescein isothiocyanate (BD Biosciences) and PI staining solution (5 µL Annexin V-fluorescein isothiocyanate, 10 µL of PI [5 µL/mL final concentration], 400 µL binding buffer).

The loss of mitochondrial membrane potential, which is indicative of apoptosis, was evaluated by measuring the fluorescence of tetramethylrhodamine ethyl ester (TMRE) dye (In Vitrogen). TMRE is a cell-permeant fluorescent dye sequestered by the active mitochondria and shows reduced staining when mitochondria are damaged. Briefly, 2.5 × 10\(^4\) BT474 cells were plated in 60-mm culture dishes, and after 48 hours of treatment with drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination of 10 nM trastuzumab and 1 µM dasatinib), TMRE (1 µM) was added to the plate for 30 minutes. Cells were treated with trypsin–EDTA solution and resuspended in 500 µL of PBS before quantification of fluorescence (excitation 488 nm, emission 570 nm) on FACScalibur flow cytometer. The data presented as a histogram differentiated between cells that preserved TMRE fluorescence (intact mitochondria or alive cells) and cells that lost TMRE fluorescence (damaged mitochondria or apoptotic cells). The percentage of cells that lost the staining is represented as the mean (95% CI) of three independent experiments.

To determine whether the combination of trastuzumab and dasatinib was synergistic, additive, or antagonist, we used the CalcuSyn v2.0 software program (Biosoft, Ferguson, MO). This program allows the calculation of the combination index based on the algorithm of Chou and Talalay (27). Combination index values less than 1 indicate synergism, values equal to 1 indicate an additive effect, whereas values greater than 1 indicate antagonism. Combination index values from three independent experiments were generated. Results were plotted as the mean (95% CI) values of duplicates from two independent experiments.

**Cell Surface Immunofluorescence**

BT474 cells were grown in DMEM with 10% of FBS, and when 80% confluent, cells were treated with drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination of 10 nM trastuzumab and 1 µM dasatinib) for 48 hours. Total RNA was extracted and purified using the PureLink Micro-to-Midi kit (Invitrogen). Double-stranded cDNA and biotinylated cRNA were synthesized using a T7-polyT primer and the BioArray RNA labelling kit (Enzo Life Sciences, Farmingdale, NY), respectively. The labeled RNA was fragmented and hybridized to human oligonucleotide arrays (HU-133 Plus 2.0) (Affymetrix, Santa Clara, CA) according to the manufacturer’s instructions. For the microarray data analysis, Affymetrix CEL files from each of the two microarray hybridization experiments for the four conditions (untreated control, 10 nM trastuzumab, 1 µM dasatinib, and a combination of 10 nM trastuzumab and 1 µM dasatinib) were imported into the dChip software (Dana Farber Cancer Institute, Boston, MA) (28). Normalization of all arrays was done against the array with median overall intensity. Genes with low expression values (<100 arbitrary units) were considered as “absent” and were discarded from the analysis. Genes with expression values greater than 100 were analyzed for differential expression in pairs of treatment conditions (control vs trastuzumab, control vs dasatinib, control vs trastuzumab and dasatinib combination, trastuzumab vs dasatinib, trastuzumab vs trastuzumab and dasatinib combination, dasatinib vs trastuzumab and dasatinib combination). The genes with greater than or equal to twofold change in expression (P < .05, Student t test two-sided) were studied using the Ingenuity Pathway Analysis software (IPA 8.6; Ingenuity Systems Inc., Redwood City, CA). This software allows functional grouping of genes according to their participation in cellular processes, such as cell cycle regulation, DNA damage, adhesion, signaling, and cell metabolism, among many others.

**Microarray Analysis of mRNA**

BT474 cells were grown in DMEM with 10% of FBS, and when 80% confluent, cells were treated with drugs (10 nM trastuzumab, 1 µM dasatinib, or a combination of 10 nM trastuzumab and 1 µM dasatinib) for 48 hours. Total RNA was extracted and purified using the PureLink Micro-to-Midi kit (Invitrogen). Double-stranded cDNA and biotinylated cRNA were synthesized using a T7-polyT primer and the BioArray RNA labeling kit (Enzo Life Sciences, Farmingdale, NY), respectively. The labeled RNA was fragmented and hybridized to human oligonucleotide arrays (HU-133 Plus 2.0) (Affymetrix, Santa Clara, CA) according to the manufacturer’s instructions. For the microarray data analysis, Affymetrix CEL files from each of the two microarray hybridization experiments for the four conditions (untreated control, 10 nM trastuzumab, 1 µM dasatinib, and a combination of 10 nM trastuzumab and 1 µM dasatinib) were imported into the dChip software (Dana Farber Cancer Institute, Boston, MA) (28). Normalization of all arrays was done against the array with median overall intensity. Genes with low expression values (<100 arbitrary units) were considered as “absent” and were discarded from the analysis. Genes with expression values greater than 100 were analyzed for differential expression in pairs of treatment conditions (control vs trastuzumab, control vs dasatinib, control vs trastuzumab and dasatinib combination, trastuzumab vs dasatinib, trastuzumab vs trastuzumab and dasatinib combination, dasatinib vs trastuzumab and dasatinib combination). The genes with greater than or equal to twofold change in expression (P < .05, Student t test two-sided) were studied using the Ingenuity Pathway Analysis software (IPA 8.6; Ingenuity Systems Inc., Redwood City, CA). This software allows functional grouping of genes according to their participation in cellular processes, such as cell cycle regulation, DNA damage, adhesion, signaling, and cell metabolism, among many others.

**Evaluation of DNA Fragmentation by Comet Assay**

Neutral comet assays that detect DNA single- and double-strand breaks (DSBs) were performed using a protocol for the single-cell gel electrophoresis assay (29). Comet assays are based on the staining of individual cellular nuclei in cells exposed to an electrophoretic field. If the nuclear DNA is intact, the image obtained is circular. If nuclear DNA suffers breaks, upon exposure to the electric field the fragmented DNA offers a characteristic “comet” appearance of the nuclei, with a head and a trailing tail. The tail length is proportional to the DNA damage. For this assay, BT474
cells were treated with drugs (10 nM trastuzumab, 1 µM dasatinib, 
or a combination of 10 nM trastuzumab and 1 µM dasatinib) for 48 
hours. After treatment, cells were suspended in 1 mL of 1% low- 
melting point agarose (Pronadisa, Madrid, Spain). Microscope 
slides were coated with 100 µL of agarose containing cells and in- 
cubated at 4°C in the dark to allow the agarose to solidify. The 
slides were placed inside a 100-mm plate and submerged in lysis 
buffer (2.5 M NaCl, 100 mM EDTA, 10 mM Tris–HCl [pH 10], 
then 0.01 (vol/vol) Triton X-100 was added overnight). After over- 
night lysis of the agarose-embedded cells, the slides were subjected 
to electrophoresis in Tris–borate–EDTA (TBE) buffer (100 mM 
Tris, 100 mM boric acid, 10 mM EDTA, pH 10) for 30 minutes at 
1.5 V/cm. The slides were stained with 80 µL ethidium bromide 
(2 µg/mL) for 5 minutes and then dipped in chilled distilled water 
to remove the excess stain. Finally, the slides were dried and DNA 
was observed at ×40 objective using an Axioplan 2 fluorescence 
microscope (Carl Zeiss Microimaging) equipped with a charge- 
coupled device camera. Fifty cells by condition (control, 10 nM 
trastuzumab, 1 µM dasatinib, combination of 10 nM trastuzumab 
and 1 µM dasatinib) were examined. Comet lengths (head plus tail, 
in micrometers) were measured with the OpenLab 5.0 (Florence, 
Italy) software, used to also acquire microphotographs.

Xenograft Studies
Female BALB/c nude mice, 7 weeks old, were obtained from 
Charles River Laboratories (Wilmington, MA). For efficient 
tumor growth, the mice (n = 6 per group) were implanted subcu- 
taneously with 1.7 mg, 60-day release, 17β-estradiol pellets 
(Innovative Research, Sarasota, FL). One week later, 1 × 10⁶ 
BT474 cells in 200 µL of DMEM and 200 µL of Matrigel 
were injected into the mammary fat pads of mice. Two weeks after 
the injection, mice (n = 6 per group) were randomly assigned into four 
groups (with equal average tumor volumes before initiation of 
treatments)—vehicle, trastuzumab, dasatinib, and drug combina- 
tion (trastuzumab and dasatinib combination). The mice were 
treated twice per week with abdominal injection of 600 µg trastu- 
zumab in PBS and/or once daily orally with 10 mg/kg dasatinib 
dissolved in 25 mM tartaric acid. Tumor diameters were serially 
measured with a digital caliper (Proinsa, Vitoria, Spain) every 
4 days, and tumor volumes were calculated using the following 
formula: 
\[ V = (L \times W^2)/2, \]
where \( V \) = volume (cubic millimeters), 
\( L \) = length (millimeters), and 
\( W \) = width (millimeters). For bio- 
chemical analyses, tumors were resected on day 28 after initia- 
tion of treatments. The mice were killed by CO₂ inhalation, and the 
tumors were resected and frozen in liquid nitrogen. Mice were 
handled at the institute’s (Servicio de Experimentación Animal, 
Salamanca, Spain) animal facility, and all treatments were in accor- 
dance with the legal and institutional guidelines.

Statistical Analysis
Comparison of continuous variables between two groups for in 
vitro assays and xenograft tumor model experiments was done 
using a two-sided Student \( t \) test. At least two independent experi- 
ments were performed for both in vitro and in vivo studies. The 
differences between different drug treatment groups were consid- 
ered to be statistically significant when the \( P \) values were less than 
.05. Means and 95% confidence intervals are reported, unless in- 
dicated otherwise. All data were analyzed using the statistical soft- 
ware SPSS 15.0 (SPSS, Inc, Chicago, IL).

Results
Effect of Trastuzumab and Dasatinib Combination on the 
Proliferation of Breast Cancer Cells
To investigate a potential synergistic effect of trastuzumab and 
dasatinib combination on the growth of breast cancer cells, we 
used two cell lines (BT474 and SKBR3) that represent in vitro 
models of HER2 receptor overexpression and activation (23), 
as well as two cell lines (MCF7 and T47D) with normal HER2 
receptor expression (27). We first checked the overexpressed 
and phosphorylated HER2 protein levels (Supplementary Figure 1, 
A and B, respectively, available online) in BT474 and SKBR3 
cells. To determine the right doses of dasatinib for use in combi- 
nation with trastuzumab, we tested the sensitivity of the breast 
cancer cell lines (BT474, SKBR3, MCF7, and T47D) to dasat- 
inib (Supplementary Figure 1, C, available online). The MTT 
metabolization results indicated that 1 µM and lower concentra-
tions of dasatinib could be used for experiments in combination 
with trastuzumab, as these doses inhibited cell proliferation and 
were within the range of clinically achievable concentrations 
(17,20). Previous studies indicated that 10 nM of trastuzumab 
represents an optimal concentration for drug combination 
studies (14).

We next investigated the effect of trastuzumab and dasatinib 
combination on the growth of breast cancer cells (Figure 1, A). In 
BT474 and SKBR3 cell lines, the drug combination had a greater 
inhibitory effect on cell growth compared with treatments with 
single-agent trastuzumab or dasatinib (BT474: trastuzumab vs 
drug combination, mean growth = 93% vs 36%, difference = 57%, 
95% CI = 42.2% to 71.7%, \( P < .001 \); dasatinib vs drug combina-
tion, mean growth = 73.5% vs 36%, difference = 37.5%, 95% 
CI = 24.9% to 50%, \( P < .002 \); SKBR3: trastuzumab vs drug 
combination, mean growth = 94.2% vs 37%, difference = 57.2%, 95% 
CI = 50.8% to 63.6%, \( P < .001 \); dasatinib vs drug combination, 
mean growth = 66.7% vs 37%, difference = 29.7%, 95% CI = 
21.8% to 37.6% (Figure 1, A). In contrast, in MCF7 and 
T47D cell lines, the drug combination did not show a greater in-
hibitory effect compared with dasatinib alone.

In BT474 cells, dasatinib enhanced the inhibitory effect of 
trastuzumab on cell growth in a dose-responsive manner (Figure 1, 
B). To analyze whether the combined effect was synergistic, we 
used the Chou–Talalay algorithm for combination index analysis 
(27) and found that low doses of dasatinib showed an additive ef-
fect with trastuzumab (0.1 µM dasatinib in combination with 
trastuzumab: combination index = 1.16, 95% CI = 1.05 to 1.27; 
0.25 µM dasatinib in combination with trastuzumab: combination 
index = 1.11, 95% CI = 1.03 to 1.19; 0.5 µM dasatinib in combina-
tion with trastuzumab: combination index = 1.05, 95% CI = 0.96 
to 1.15), whereas 1 µM of dasatinib in combination with trastu-
zumab showed a strong synergistic effect (combination index = 
0.44, 95% CI = 0.30 to 0.58) (Figure 1, C). 

Trastuzumab and dasatinib combination also affected the mor-
phology of BT474 cells. In culture dishes, BT474 cells grow as 
monolayers and form island-like clusters. The drug combination 

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Figure 1. Effect of trastuzumab and dasatinib combination on the proliferation of breast cancer cells. A) BT474, SKBR3, MCF7, and T47D cells were cultured in the presence of trastuzumab (10 nM) or dasatinib (1 µM) or a combination of both drugs, and 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) metabolism was measured. Briefly, cells were treated with the indicated drugs, and after 3 days, MTT was added. Absorbance was measured at 570 nm. The mean absorbance values of untreated samples from each cell line were taken as 100%. Absorbance values of the cells treated with different drugs are plotted as percentages with respect to the mean value of the untreated samples. Means and 95% confidence intervals of an experiment representative of three independent experiments performed in quadruplicate are shown. In BT474: *$P < .001$, trastuzumab vs drug combination; #P = .002, dasatinib vs drug combination. In SKBR3: †$P < .001$, trastuzumab vs drug combination; ‡$P < .001$, dasatinib vs drug combination. Student $t$ test (two-sided) was used to compare means between groups and to calculate $P$ values. B) Dose–response analysis of dasatinib on the proliferation of BT474 cells treated with trastuzumab. Cells were treated with trastuzumab (10 nM) in combination with different doses (0.1, 0.25, 0.5, or 1 µM) of dasatinib, and MTT metabolism was measured after 3 days. Control cells were untreated. The results show the means and 95% confidence intervals of an experiment, performed two independent times in quadruplicate. C) The combination index values were calculated using the CalcuSyn software. The graph shows the means and 95% confidence intervals of two independent experiments performed in triplicate. D) Effect of trastuzumab, dasatinib, and the drug combination on the morphology of BT474 cells grown as monolayers (top panels) or as three-dimensional (3D) cultures (bottom panels). To assess the effect of different drugs on the morphology of BT474 cell monolayers (top panels), 5 x 10⁵ cells were plated in 100-mm dishes, allowed to adhere for 24 hours, then trastuzumab (10 nM), dasatinib (1 µM), or a combination of both drugs were added. The images were taken after 48 hours. To assess the effect of different drugs on BT474 cells grown as 3D cultures, 5 x 10³ cells were grown in semisolid media for 10 days and then treated with trastuzumab (10 nM), dasatinib (1 µM), or a combination of both drugs, for an additional 7 days (bottom panels). All images were taken at x25 magnification. Scale bar = 50 µm. E) Bar graph representation of the sphere diameters in 3D cultures. BT474 cells grown as 3D cultures were treated with trastuzumab (10 nM), dasatinib (1 µM), or a combination of both drugs. The diameter of the spherical cells (plotted as arbitrary units) after treatment with drugs is shown as means and 95% confidence intervals. Means were compared using the Student $t$ test (two-sided). *$P < .001$, trastuzumab vs drug combination; #P < .001, dasatinib vs drug combination.
caused a contraction of these islands, and the contours of the cells were difficult to delineate (Figure 1, D, top panels). We also explored whether the trastuzumab and dasatinib combination affected the three-dimensional growth of BT474 cells. For these experiments, BT474 cells were cultured in Matrigel, a semisolid media in which they form spherical structures. Treatment with the drug combination showed a substantial decrease in the diameter of these spheres, which was not appreciable when cells were treated with the individual agents (trastuzumab vs drug combination, mean diameter = 2.85 vs 1.55 arbitrary units, difference = 1.3 arbitrary units, 95% CI = .96 to 1.63 arbitrary units, P < .001; dasatinib vs drug combination, mean diameter = 2.76 vs 1.55 arbitrary units, difference = 1.21 arbitrary units, 95% CI = .82 to 1.59 arbitrary units, P < .001) (Figure 1, D, bottom panels, and E).

We also explored whether dasatinib could enhance the action of other drugs used in the therapy of breast cancer. Dasatinib did not substantially increase the antitumoral effect of gemcitabine in BT474 (Supplementary Figure 2, A, available online) and SKBR3 (Supplementary Figure 2, B, available online) cells. However, combination of dasatinib with taxotere or vinorelbine had a higher antitumoral effect than treatment with the individual drugs. Interestingly, addition of trastuzumab to these combinations (dasatinib and gemcitabine, dasatinib and taxotere, dasatinib and vinorelbine) showed augmented antitumoral efficacy.

**Coordinated Effects of Trastuzumab and Dasatinib on HER Signaling**

To investigate the mechanism responsible for the biological activity of trastuzumab and dasatinib combination, we explored the biochemical changes in both single and combined treatments. Because trastuzumab and dasatinib inhibit tyrosine kinases (8,21), we analyzed their effect on tyrosine phosphorylation in an antibody array containing a panel of 42 different RTKs, including the ones targeted by these drugs. These experiments showed that the most phosphorylated RTKs in BT474 cells corresponded to HER receptors, especially HER2 and HER3 (Figure 2, A). Trastuzumab decreased the level of phosphorylated HER2, but dasatinib had no substantial effect on the amount of phosphorylated HER2. However, trastuzumab and dasatinib combination strongly decreased phosphorylated HER2 and phosphorylated HER3 levels. The drug combination showed analogous results in SKBR3 cells, and both phosphorylated HER2 and phosphorylated HER3 levels were decreased (Supplementary Figure 3, A, available online). Observations were confirmed by immunoprecipitation.
and immunoblotting experiments, and it was also observed that there was a decrease in the total amount of HER2 and HER3 after treatment with the drug combination (Figure 2, B, and Supplementary Figure 3, A, available online). The decrease in HER2 tyrosine phosphorylation induced by the drug combination was also evidenced by immunofluorescence microscopy, and an overall decrease in HER2 on the cell surface was also noted (Figure 2, C). The latter finding was also substantiated by cell surface biotinylation of HER2 proteins (Supplementary Figure 3, B, available online). The combined treatment did not substantially affect the amount of EGFR, although a small decrease in phosphorylated EGFR was detected (Figure 2, B, and Supplementary Figure 3, A, available online).

We reasoned that if the combined treatment with trastuzumab and dasatinib affected tyrosine phosphorylation of HER receptors, the signaling pathways activated by these receptors would consequently experience an analogous impact. Therefore, we investigated the effect of individual drugs and drug combination on RAS-RAF-MEK-ERK1/2 and phosphatidylinositol 3-kinase–AKT activation pathways, given the important role of these pathways in HER signaling. In addition, we also explored the tyrosine phosphorylation status of the cytosolic itinerant tyrosine kinases c-SRC and FAK, which are well-known dasatinib targets (21). In the resting state of phosphorylation, dasatinib inhibited the dual phosphorylation of ERK1 and tyrosine phosphorylation of c-SRC and FAK (Figure 2, D). The inhibitory effect of trastuzumab and dasatinib combination on phosphorylation was analogous to that of dasatinib, indicating that the activity of combined drugs on these signaling mediators reflect the activity of dasatinib alone. Similar to the effect of the drugs on HER receptors, treatment with the drug combination inhibited the phosphorylation of the adaptor protein SHC1, AKT, as well as a downstream substrate of AKT—the 70 kDa S6 protein kinase (p70S6K). Treatment with individual drugs did not affect the constitutive resting state phosphorylation of these proteins.

Gene Expression Profiling and DNA Damage in Cells Treated With Trastuzumab and Dasatinib

In addition to the biochemical studies, we also performed mRNA expression profiling of BT474 cells treated with trastuzumab, dasatinib, or trastuzumab and dasatinib combination using oligonucleotide arrays. The expression of several genes was altered in response to treatment with the single drugs, but more genes showed altered expression after trastuzumab and dasatinib combination treatment (Figure 3, A). Trastuzumab modified the expression of 181 genes; dasatinib modified the expression of 193 genes; and the drug combination modified the expression of 263 genes. The expression of some genes was modified only by the drug combination and not by individual drugs (Figure 3, A). The drug combination modified the expression of genes involved in cell cycle regulation and DNA recombination and/or repair. Among the most notable cell cycle regulators, whose expression was modified by the drug combination, were CDK2, cyclin E1, cyclin E2, cyclin B1, and p21 (Figure 3, B). The differential expression was statistically significant for all genes shown in the figure (P < .05). A time-course analysis of different protein levels demonstrated that the level of p21 decreased within 12 hours, CDK2 and cyclin E1/2 decreased within 36 hours, and cyclin B1 decreased within 24 hours of treatment with the drug combination (Figure 3, C). In contrast, the level of p27, an important negative regulator of cell cycle progression in BT474 cells (30), was substantially increased by the combined treatment of trastuzumab and dasatinib.

Treatment with the drug combination also modified the expression of genes that participate in DNA damage responses (Figure 3, B). This result led us to explore whether treatment with trastuzumab and dasatinib triggered a DNA damage response. Of the many types of DNA damage, the most toxic is DNA DSBs (31,32). The DNA lesions are repaired mainly through nonhomologous end joining or homologous recombination (31). Because RAD51 recombines, one of the genes whose expression was modified by the combined drug treatment, is involved in homologous recombination, we first investigated whether the drug combination triggered DSBs. Comet assays indicated that treatment of BT474 cells with the drug combination induced the characteristic “comet” appearance of the nuclei, whereas the individual drugs showed no such effect (Figure 3, D).

Upon generation of DSBs, the MRE11A–RAD50–NBS1 (MRN) protein complex is recruited to the sites of the DNA lesions, which triggers the activation of kinases such as ataxia telangiectasia mutated that phosphorylate several downstream mediators (32). One of these downstream molecules is the phosphorylated form of histone H2AX (known as γH2AX), which is used as a surrogate marker for the quantitation of DSBs (33). Immunoblot results showed that γH2AX was detected in cells treated with trastuzumab and dasatinib but not in cells treated with the individual drugs (Figure 3, E). A time-course analysis performed to define the effects of trastuzumab and dasatinib on proteins that participate in the DSB repair pathway verified that the levels of RAD1, RAD51, and RAD54B were substantially decreased by the drug combination (Figure 3, C), and this decrease coincided with the increase in level of γH2AX. The combined drug treatment also increased the level of GADD45γ, which is involved in the DSB repair pathway. The levels of MRE11A and RAD50, both constituents of the MRN complex, were unaffected by trastuzumab and dasatinib combination treatment.

Effect of Trastuzumab and Dasatinib Combination on Apoptosis

The decrease in MTT metabolism in cells treated with dasatinib and trastuzumab could be because of reduced proliferation, cell death, or both. Moreover, the genomic and biochemical studies indicated deregulation of proteins that control these biological processes. Therefore, next we investigated the effect of different drug treatments on cell cycle and apoptosis. In BT474 cells, PI staining revealed a pattern of DNA staining, characterized by a large G0/G1 peak of interphase cells (2n DNA content), a much smaller G2/M peak of cells with duplicated DNA content (4n), and an intermediate subpopulation that corresponded to the S phase (Figure 4, A). Treatment with the individual drugs did not have a substantial effect on the distribution of the different cell cycle phases. However, treatment with the drug combination profoundly affected the PI staining of BT474 cells, which impaired accurate analyses of the action of the drug combination on the different cell cycle phases. We observed that the G0/G1 and...
G2/M peaks decreased in height, and the relative number of cells in the S phase increased. This can be caused by lower sensitivity of S phase cells to the action of the drug combination. An important accumulation of sub-G0 staining was observed in cells treated with the drug combination. As this latter characteristic (ie, accumulation of sub-G0 cells) is indicative of cell death (34), we assessed whether treatment with trastuzumab and dasatinib combination triggered apoptosis in breast cancer cells. Annexin V-fluorescein isothiocyanate staining showed that the number of apoptotic cells was elevated in BT474 cells treated with the drug combination (trastuzumab and dasatinib combination).
Apoptosis may be caused by the loss of membrane potential and increased permeability of the mitochondrial outer membrane (MOM) (35). Analysis of MOM potential indicated that the drug combination affected the membrane potential of a greater number of cells compared with the individual drugs (control vs drug combination). Cells were treated with drugs and caspase inhibitors, either individually, or simultaneously, as indicated in the figure. The following concentrations were used: TRAIL (1 nM, combined with 1 µg/mL of cycloheximide to increase the activity of TRAIL), caspase-8 inhibitor (Z-IETD-FMK, 1 µM), caspase 9 inhibitor (Z-LEHD-FMK, 1 µM), and pancaspase inhibitor (Z-VAD-FMK, 1 µM). The cells were stained with Annexin V and analyzed by flow cytometry. The bar graph represents the mean percentage of Annexin V-positive cells from three independent experiments. Ninety-five percent confidence intervals are also shown. Control cells were untreated. Dasat = dasatinib; TRAIL = tumor necrosis factor–related apoptosis-inducing ligand; Trast = trastuzumab.

The levels of these proteins were not substantially affected after treatment with trastuzumab or dasatinib alone; however, the levels were almost undetectable after treatment with the drug combination. In addition, the levels of phosphorylated BAD (a downstream target of AKT) and BIRC2 also decreased after treatment with the drug combination (Figure 4, D).

To investigate whether a caspase-dependent or independent signaling pathway was involved in apoptosis (36), we assessed the levels of caspase-3, -8, and -9, on treatment with trastuzumab or dasatinib as single drugs, as well as the drug combination (Figure 4, E). Treatment with trastuzumab and dasatinib combination showed a decrease in the level of all three procaspases. It is noteworthy that we were unable to detect the cleaved (active) fragments of these caspases in cells treated with the drug combination. However, when apoptosis was induced in BT474 cells with tumor necrosis factor–related apoptosis-inducing ligand (TRAIL), activation of caspases via generation of cleaved fragments was evident (data not shown).

dasatinib combination, 51.4%) compared with cells treated with the individual drugs (trastuzumab, 2%; dasatinib, 6.9%) (Figure 4, B).
Discussion

In this study, we showed that the combination of trastuzumab with dasatinib was highly effective against breast cancer cells overexpressing HER2 receptors. Both drugs individually inhibited cell proliferation in vitro and exhibited antitumoral action, but their combination showed a more potent effect on HER2-overexpressing cells. However, compared with single drugs, treatment with the drug combination did not show a greater inhibition of proliferation in cells with normal expression of HER2 receptors. We confirmed these observations in vivo in a mouse mammary fat pad model of breast cancer. Treatment of tumor-bearing mice with the drug combination showed a stronger inhibitory effect on tumor growth than treatment with single drugs. We further demonstrated that there was a complete regression of tumors, even large tumors, in mice treated with the drug combination. In addition, discontinuation of the treatment for 9 months did not result in tumor recurrence.

The mechanistic studies indicated that the drug combination strongly decreased the levels of phosphorylated HER2 and phosphorylated HER3, which were accompanied by a decrease in the total amount of these receptors. We explored whether the combined treatment affected the downstream signaling routes, such as the ERK1 or AKT pathways that regulate cell proliferation and survival (37,38). Dasatinib had the same inhibitory effect on the phosphorylated levels of ERK1 as the combined drug treatment. Therefore, the exclusive inhibition of ERK1 cannot explain the effects of the combined drug treatment on cell proliferation and cell death. Analogously, treatment with dasatinib inhibited SRC or FAK phosphorylation to the same degree as the combined drug treatment. These two kinases are known targets of dasatinib (21) and have been reported to participate in several oncogenic processes (39). We noted that the combined treatment, but not the individual drugs, decreased the level of phosphorylated AKT. Downstream targets of AKT such as p70S6K and BAD were also affected by the combined drug treatment, but not by the individual drugs, as the resting phosphorylated levels of these proteins were reduced on treatment with trastuzumab and dasatinib. The inhibition of different signaling pathways suggests that the synergistic antitumoral action of the combined drug treatment may result from the sum of the inhibition of multiple signaling routes involved in the control of cell proliferation and survival.

Our results showed that the drug combination also affected important regulators of cell cycle progression and a group of proteins involved in DNA repair and/or recombination. Moreover, the drug combination induced DNA DSBs and a DNA damage response that was evidenced by the phosphorylation of H2AX protein. DNA damage can induce cell cycle arrest through activation of kinases such as ataxia telangiectasia mutated (ATM), ataxia telangiectasia and RAD3-related kinase (ATR), and the CHK checkpoint homolog 1 or 2 kinases (CHEK1 or CHEK2, respectively) that reduce CKD activity by various mechanisms (32). The decrease in CDK activity may provoke arrest of cell cycle progression at the G1–S or G2–M checkpoints, which are thought to increase the time available for DNA repair.

The drug combination also induced caspase-independent apoptosis. This was supported by the lack of any effect of the caspase

Efficacy of Trastuzumab and Dasatinib Combination on Tumor Growth In Vivo

To determine whether the synergistic action of the drug combination was also observed in vivo, we implanted BT474 cells into the mammary fat pad of mice randomly assigned to the following four groups—untreated control, dasatinib, trastuzumab, or a combination of trastuzumab and dasatinib. The tumors continued to grow in the untreated group (Figure 5, A), and by day 28 of follow-up, the mice were killed because of the large size of their tumors. In agreement with the in vitro results, the combination of trastuzumab and dasatinib showed a superior antitumoral effect compared with either drug alone (control vs combination, mean volume = 2.6 vs 0.5 cm3, difference = 2.1 cm3, 95% CI = 0.76 to 3.51 cm3, P = .010; trastuzumab vs combination, mean tumor volume = 1.5 vs 0.5 cm3, difference = 1.0 cm3, 95% CI = 0.12 to 1.93 cm3, P = .032; dasatinib vs combination, mean volume = 1.48 vs 0.5 cm3, difference = 0.98 cm3, 95% CI = 0.50 to 1.45 cm3, P = .003) (Figure 5, B). It is noteworthy that the tumors from mice treated with the drug combination showed regression, whereas tumors from mice treated with the individual drugs showed stability in size or slight growth (Figure 5, A and B). Because of the strong antitumoral effect of the drug combination, we decided to maintain two mice from this group to follow the evolution of the tumors. In these mice, treatment with trastuzumab and dasatinib combination resulted in complete regression of the tumors by day 36, and the tumors did not relapse at the site of injection even after discontinuation of the treatment for a long period of time (Figure 5, C).

Tumor samples were also analyzed for the phosphorylation levels of HER receptors, as well as the levels of DNA damage response proteins. The combined drug treatment showed a decrease in the level of phosphorylated HER2 compared with control mice or mice treated with the individual drugs (Figure 5, D). The combined drug treatment also showed a decrease in the levels of RAD1, RAD51, RAD54B, and an increase in the level of γH2AX (Figure 5, E).
inhibitors on apoptosis induced by the drug combination. One of the possible mediators in caspase-independent apoptosis is NAIF1, a protein that is released from the mitochondrial intermembrane space by certain apoptotic stimuli. The release of NAIF1 from the mitochondria to the cytosol, on treatment with the drug combination, indicated that this mechanism could be responsible for caspase-independent apoptosis.

The fact that the drug combination severely affected the DNA repair machinery and led to the accumulation of DSBs raises some questions regarding the mechanism of control of DNA repair machinery by tyrosine kinases and the potential clinical implications. The time-course studies showed a decrease in the level of RAD51 protein, sequentially followed by an accumulation of γH2AX protein. It is possible that the decrease in the level of RAD51 protein impedes adequate repair of spontaneous DNA lesions, and accumulation of such lesions triggers a DNA damage response that results in apoptosis. If that is the case, it is possible that the integrity of the homologous recombination machinery is critically controlled by the interplay of tyrosine kinases sensitive to trastuzumab and dasatinib. In support of our hypothesis, a recent report showed that erlotinib, an inhibitor of EGFR, blocked homologous recombination repair of the DSBs in breast cancer cells through reduction of RAD51 foci formation (40). Previous studies have also indicated that RTKs may regulate DNA repair (41,42). Gefitinib, another EGFR inhibitor, was shown to impede DNA repair in response to ionizing radiations in macrocytic lung cancer cells (41). The mutated forms of MET protein, an RTK implicated in several oncogenic processes such as invasion and metastasis (43) or drug resistance (44), have been reported to bind to and phosphorylate RAD51, facilitating DNA repair in tumor cells (42). Recently, the Williams–Beuren syndrome transcription factor (WSTF; also known as BAZ1B), a tyrosine kinase that is a component of the WICH complex (WSTF-ISWI ATP-dependent chromatin-remodeling complex), has been shown to regulate the DNA damage response through phosphorylation of Tyr142 of H2AX (45).

From the clinical point of view, the fact that trastuzumab and dasatinib combination induced DNA damage in HER2-overexpressing cells in this study, opens up the possibility of combining these drugs in the treatment of HER2-positive breast cancers. In this context, we showed that dasatinib may enhance the activity of treatments for breast cancer that are currently used in the clinics to...
treat HER2-positive patients. In addition, our results also offer the interesting option of using dasatinib with other antineoplastic agents in tumors that may be particularly sensitive to DNA damaging drugs or radiotherapy. Interestingly, in head and neck cancer, a radiosensitive tumor, in vitro studies have shown antitumor activity of agents that target SRC combined with gefitinib (22). Also, the effectiveness of anti-EGFR therapies in colon cancer opens the possibility of exploring whether dasatinib synergizes with anti-HR drugs or radiotherapeutic treatments in these pathologies.

Our study may have a few limitations. Although, the promising findings of this preclinical study indicate potential clinical benefits, we cannot predict the effectiveness or toxicity of the drug combination in humans. Of note, analysis of the antiproliferative effect of the drug combination using the Chou–Talalay algorithm indicated that the lower doses of dasatinib (0.1, 0.25, and 0.5 µM) were additive to trastuzumab, whereas the dose of 1 µM showed synergistic effect. The latter is an achievable concentration (20), but the fact that the synergistic effect was observed at a high concentration of dasatinib should be taken into account for the adequate design of clinical trials.

References


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**Affiliations of authors:** Instituto de Biología Molecular y Celular del Cáncer, CSIC-Universidad de Salamanca, Salamanca, Spain (SS, JCM, AP); Servicio de Oncología Médica, Complejo Hospitalario Universitario de Albacete, AECC Unit, Albacete, Spain (AO).